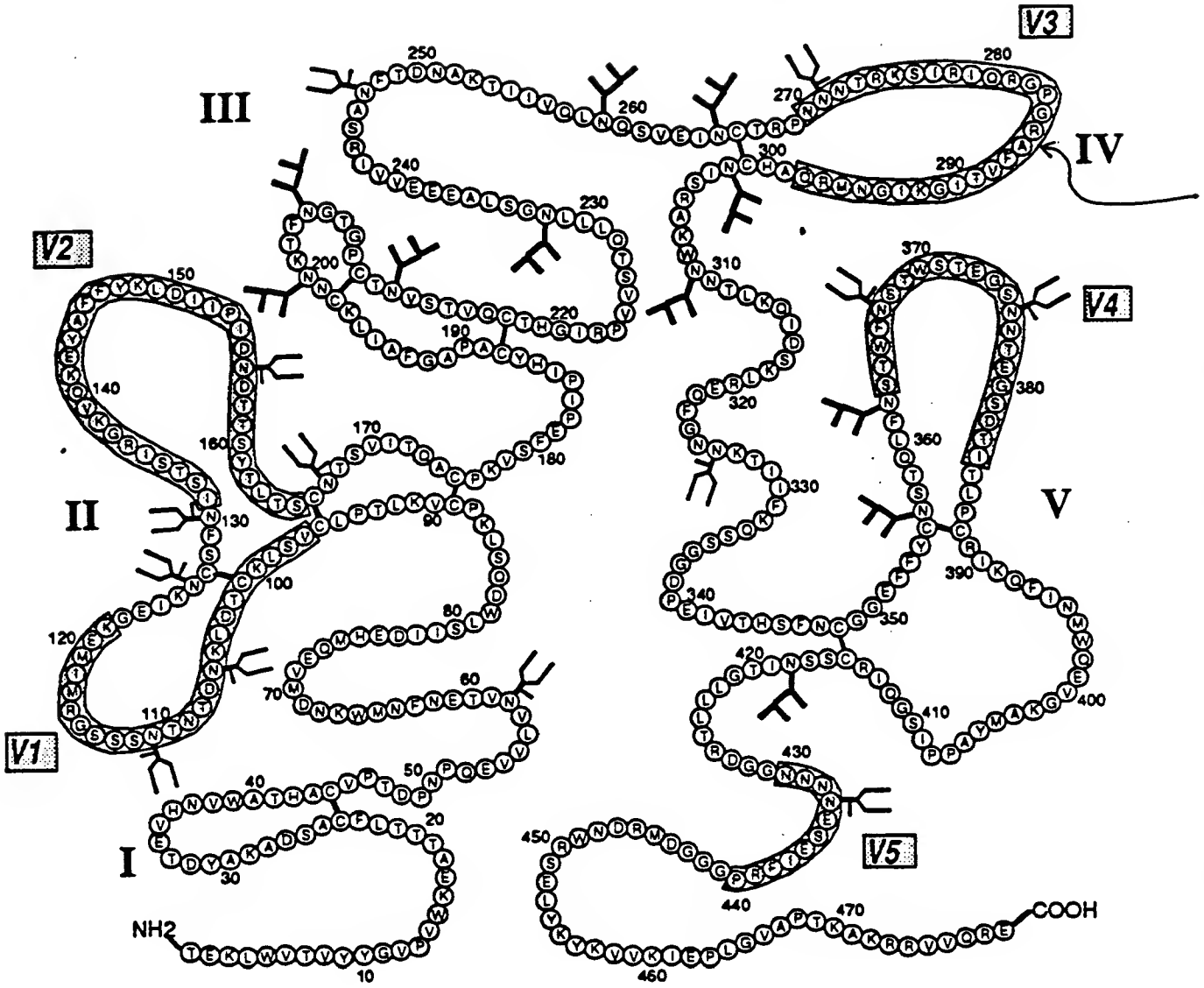


Fig. 1

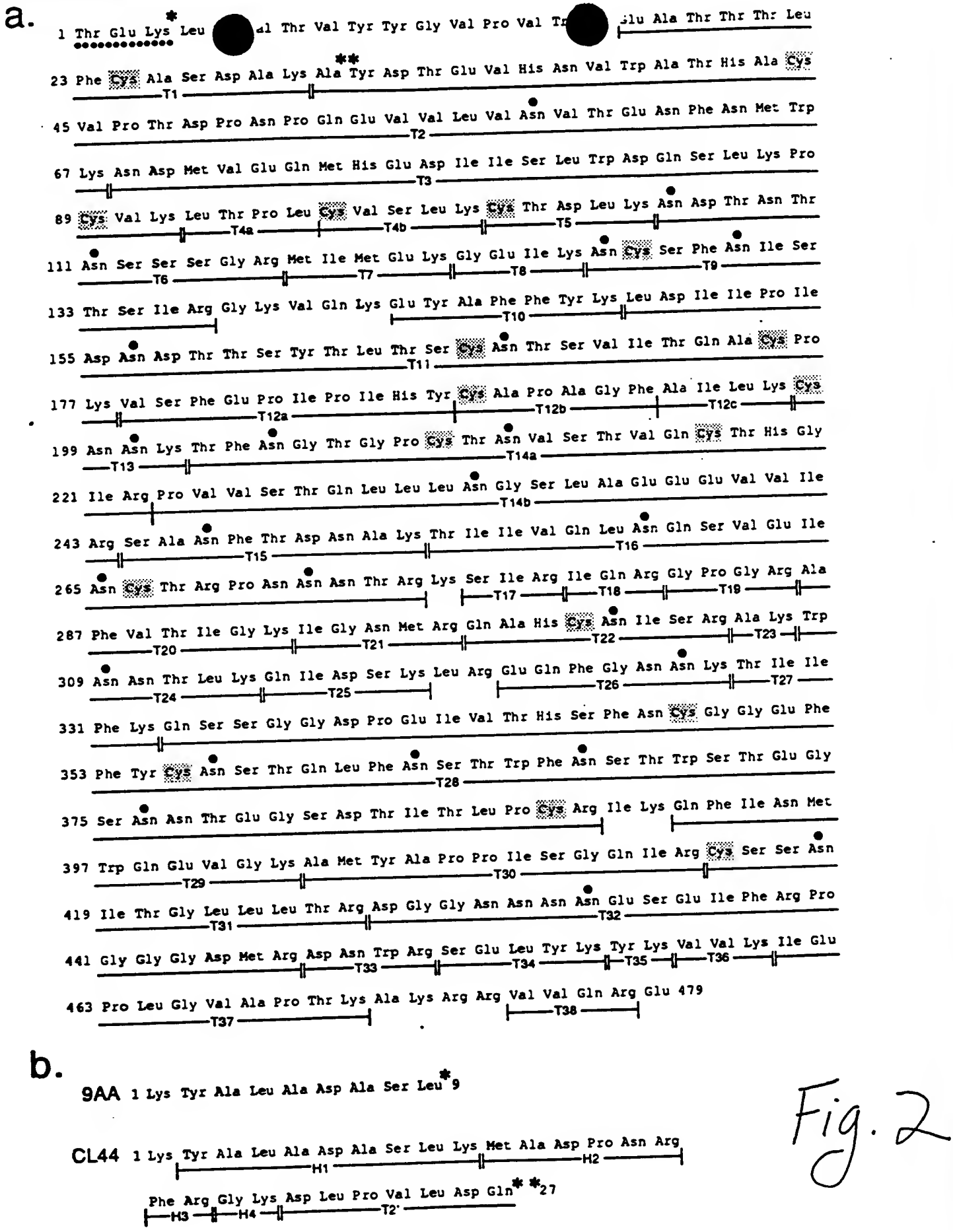
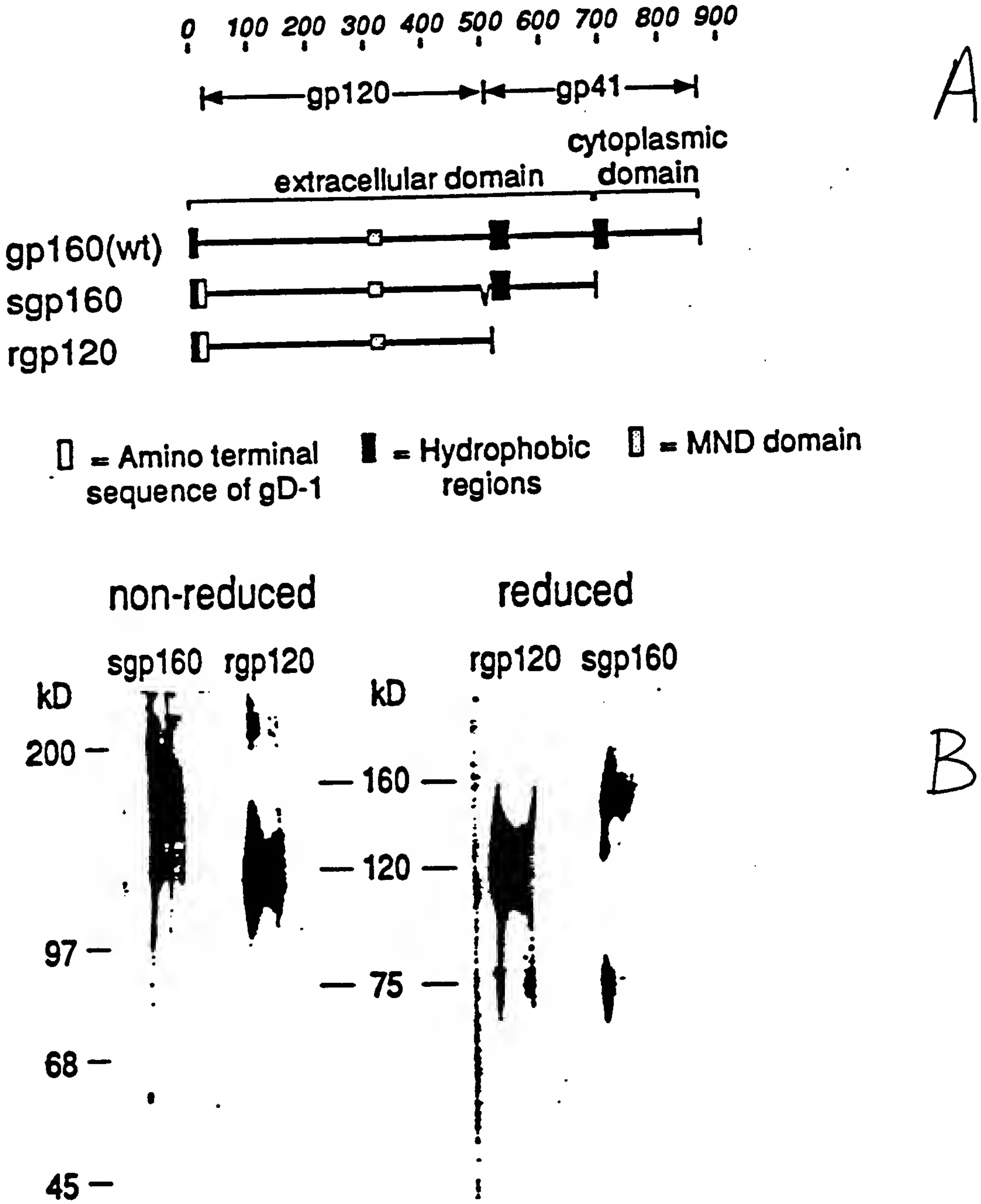

a.
1 Thr Glu Lys Leu
Thr Val Tyr Tyr Gly Val Pro Val
Glu Ala Thr Thr Thr Leu
23 Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys
T1
45 Val Pro Thr Asp Pro Asn Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
T2
67 Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu Lys Pro
T3
89 Cys Val Lys Leu Thr Pro Leu Cys Val Ser Leu Lys Cys Thr Asp Leu Lys Asn Asp Thr Asn Thr
T4a
T4b
T5
111 Asn Ser Ser Ser Gly Arg Met Ile Met Glu Lys Gly Glu Ile Lys Asn Cys Ser Phe Asn Ile Ser
T6
T7
T8
T9
133 Thr Ser Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Phe Phe Tyr Lys Leu Asp Ile Ile Pro Ile
T10
155 Asp Asn Asp Thr Thr Ser Tyr Thr Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro
T11
177 Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys Cys
T12a
T12b
T12c
199 Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly
T13
T14a
221 Ile Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile
T14b
243 Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu Asn Gln Ser Val Glu Ile
T15
T16
265 Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Arg Ile Gln Arg Gly Pro Gly Arg Ala
T17
T18
T19
287 Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Asn Ile Ser Arg Ala Lys Trp
T20
T21
T22
T23
309 Asn Asn Thr Leu Lys Gln Ile Asp Ser Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile
T24
T25
T26
T27
331 Phe Lys Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe
353 Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Phe Asn Ser Thr Trp Ser Thr Glu Gly
T28
375 Ser Asn Asn Thr Glu Gly Ser Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Phe Ile Asn Met
397 Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile Arg Cys Ser Ser Asn
T29
T30
419 Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Asn Asn Asn Glu Ser Glu Ile Phe Arg Pro
T31
T32
441 Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu
T33
T34
T35
T36
463 Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu 479
T37
T38
b.
9AA 1 Lys Tyr Ala Leu Ala Asp Ala Ser Leu 9
CL44 1 Lys Tyr Ala Leu Ala Asp Ala Ser Leu Lys Met Ala Asp Pro Asn Arg
H1
H2
Phe Arg Gly Lys Asp Leu Pro Val Leu Asp Gln 27
H3
H4
T2'

Fig. 2

Fig. 3



A
0 100 200 300 400 500 600 700 800 900
gp120
gp41
cytoplasmic domain
extracellular domain
gp160(wt)
sgp160
rgp120
= Amino terminal sequence of gD-1
= Hydrophobic regions
= MND domain
B
non-reduced
reduced
sgp160 rgp120
rgp120 sgp160
kD
200
97
68
45
kD
160
120
75

Fig. 4

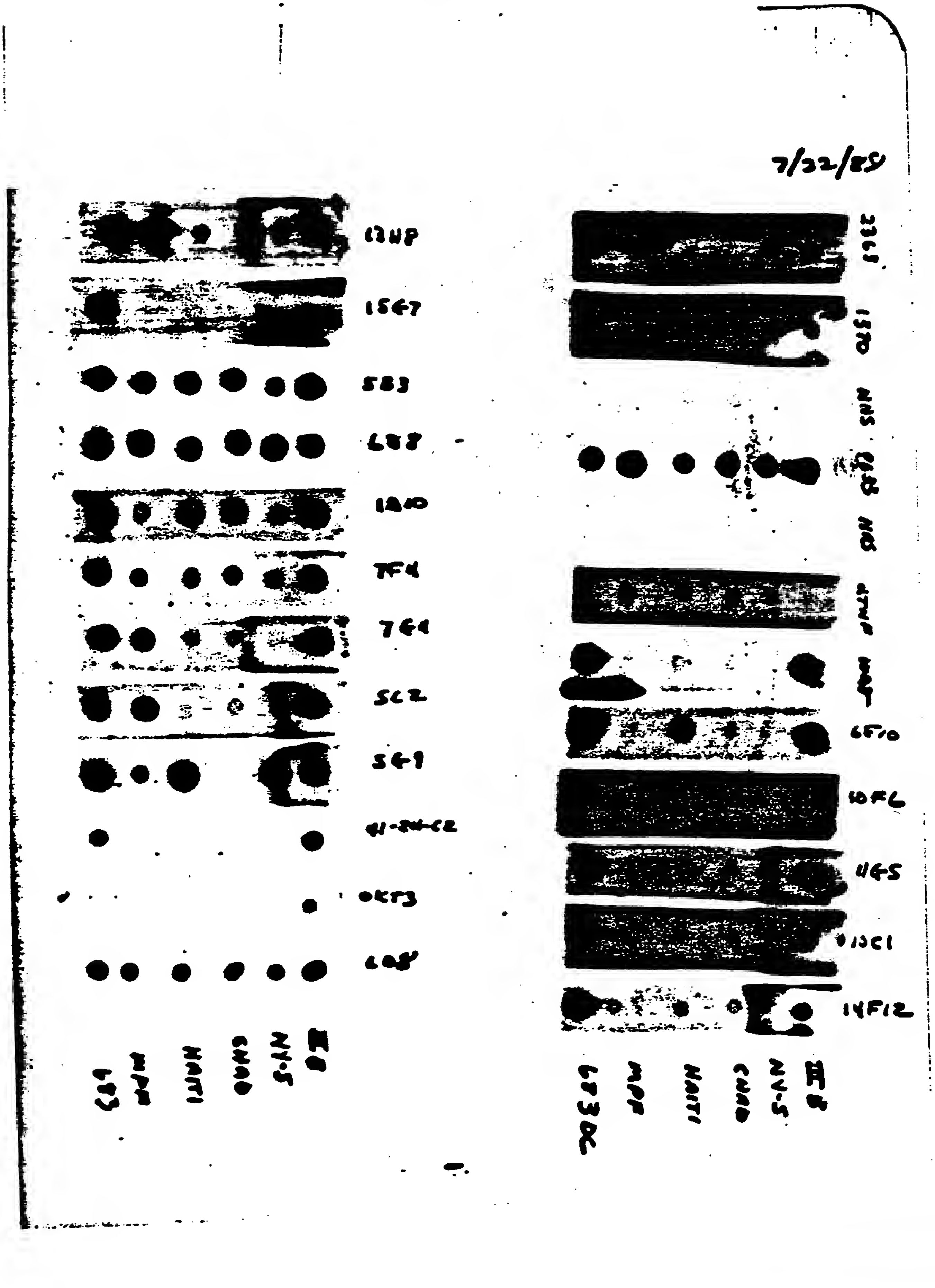


Fig. 5

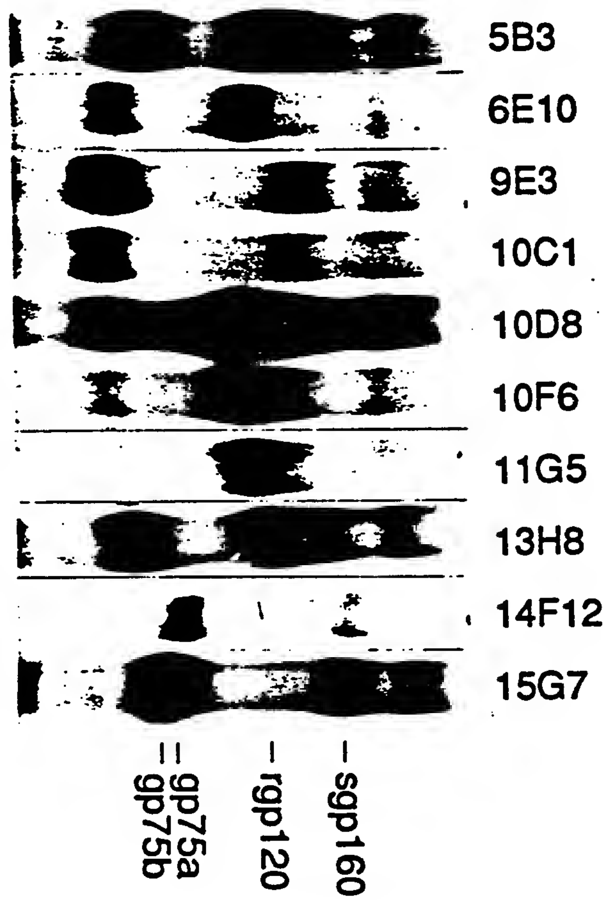
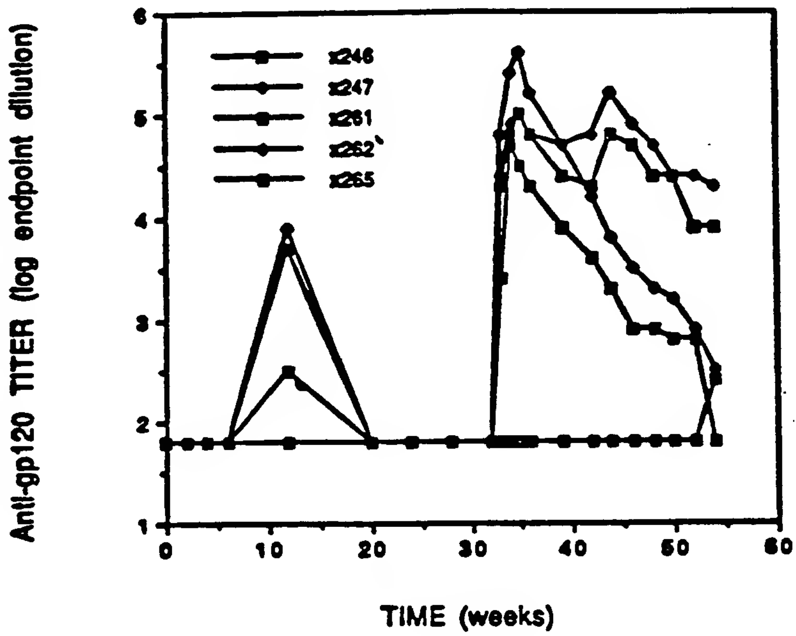
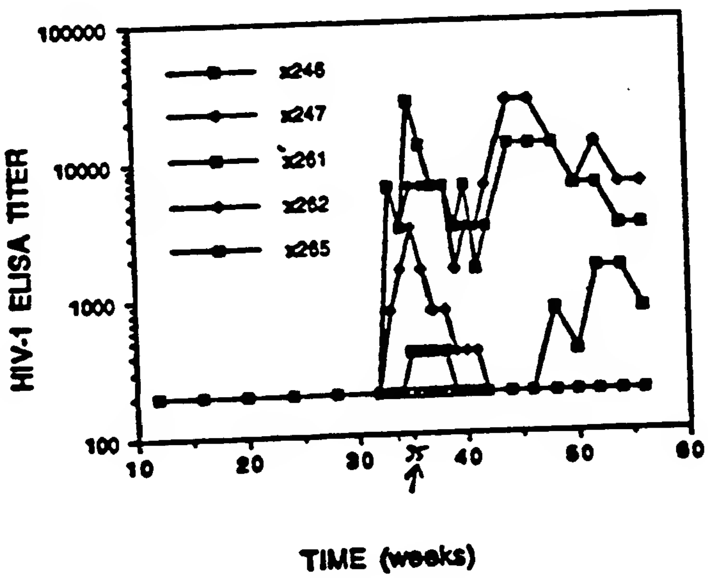


Fig. 6

Chimp Study 2: Anti-gp120 Titers



A



B

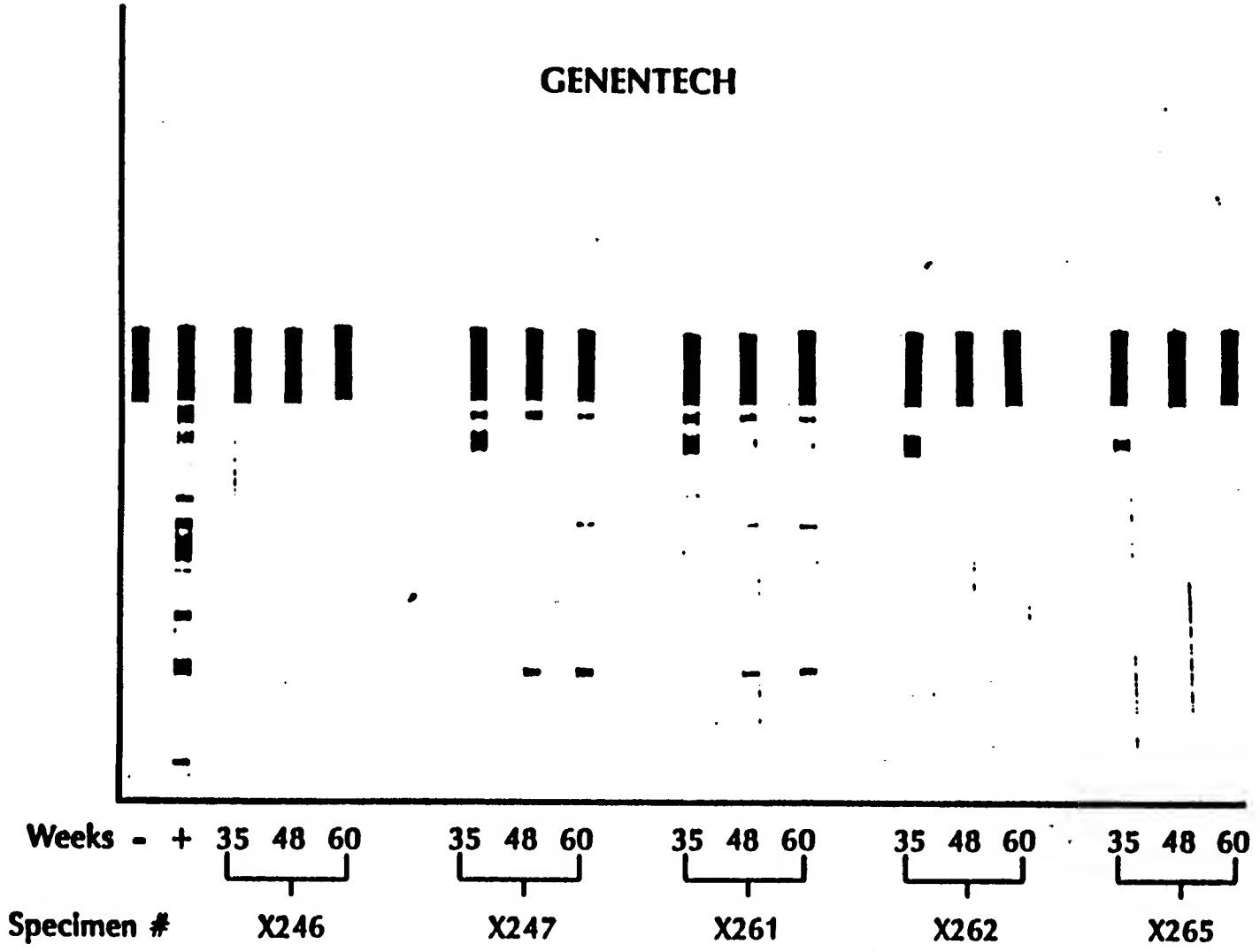
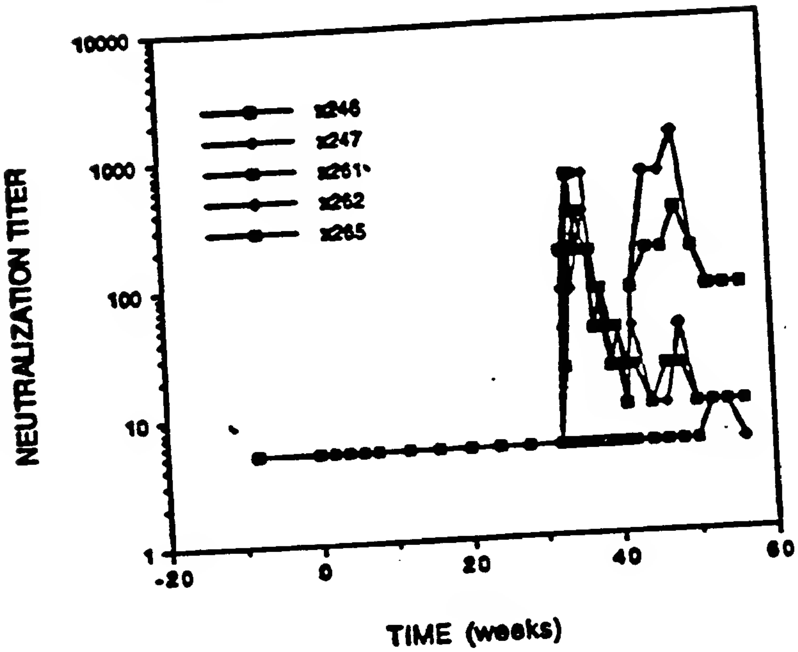


Fig. 1

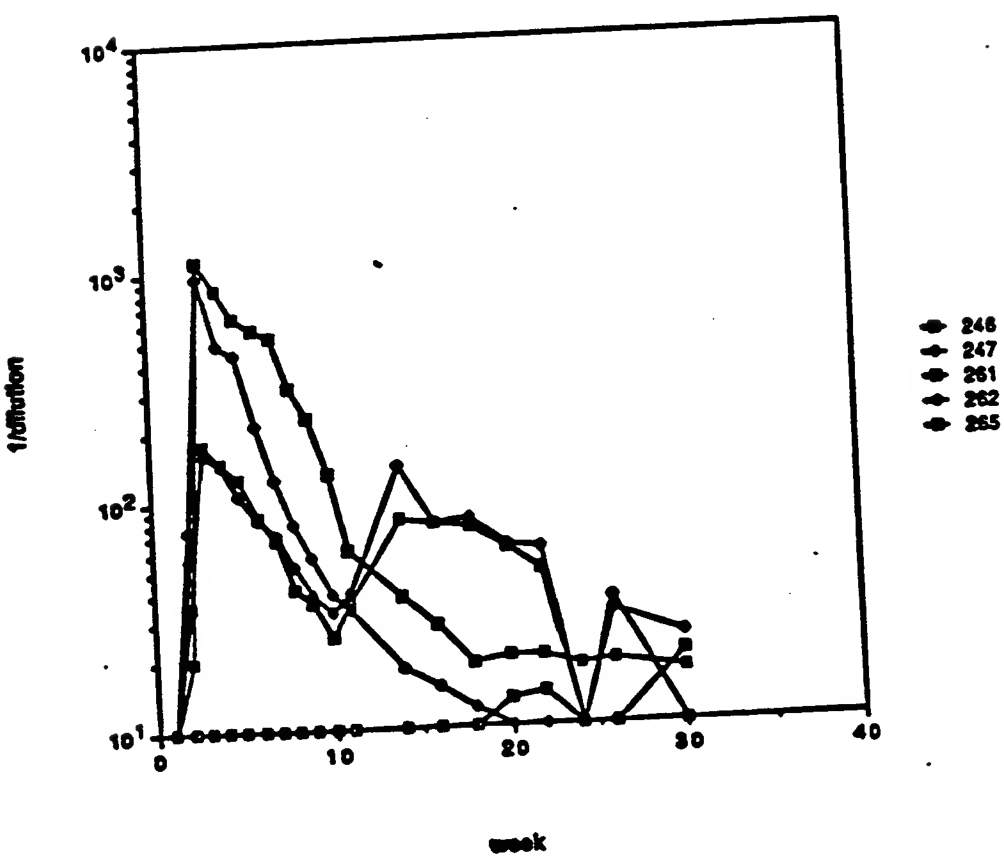
Fig. 8

Data from "chimp neuts summary"



A

ANTI RP135 TITER AT 0.9 O.D. 492 ELISA



B